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49321-120.ST25.txt
SEQUENCE LISTING

<110> Oregon Health & Science University
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Nelson, Jay
Fruh, Klaus
King, Jeff
Jelinek, Laura
Hirsch, Alec
DeFilippis, Victor

<120> METHODS OF TREATMENT AND DIAGNOSIS USING MODULATORS OF
VIRUS-INDUCED CELLULAR GENE SEQUENCES

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<141> 2004-04-15

<150> US 60/486,694

<151> 2003-07-11

<150> US 60/533,103

<151> 2003-12-29

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<170> PatentIn version 3.2

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 Asn Ala His Ala Gly His Ser Gly Leu Leu His Gly Pro Ala Ser Arg
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 atg agc ctc ccc aat tcc tcc tgc ctc tta gaa gac aag atg tgt gag 226
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Pro Ile Leu Gly Trp Asn His Phe Met Gln Gln Thr Ser Val Arg Arg
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Glu Asp Lys Cys Glu Thr Asp Phe Tyr Asp Val Thr Trp Phe Lys Val
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 Gly Gly Leu Thr Asp Lys Leu Thr Gln Ala Gln Ile Phe Asp Tyr Ser
 40 45 50
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 Glu Ile Pro Asn Phe Pro Arg Ser Thr Val Pro Gly His Ala Gly Arg
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 Arg Phe His Met Tyr Glu Gly Tyr Pro Leu Trp Lys Val Thr Phe Pro
 85 90 95
 gtg agg gtt ttc cac ctt ctg ggt gtg gac acc ctg gta gtc acc aat 454
 Val Arg Val Phe His Leu Leu Gly Val Asp Thr Leu Val Val Thr Asn
 100 105 110 115
 gca gca gga ggg ctg aac ccc aag ttt gag gtt gga gat atc atg ctg 502
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 120 125 130
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 Ile Arg Asp His Ile Asn Leu Pro Gly Phe Ser Gly Gln Asn Pro Leu
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Gln Met Gly Glu Gln Arg Glu Leu Gln Glu Gly Thr Tyr Val Met Val
180 185 190 195

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200 205 210

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215 220 225

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230 235 240

aag gtc atc atg gat tat gaa agc ctg gag aag gcc aac cat gaa gaa 886
Lys Val Ile Met Asp Tyr Glu Ser Leu Glu Lys Ala Asn His Glu Glu
245 250 255

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Val Leu Ala Ala Gly Lys Gln Ala Ala Gln Lys Leu Glu Gln Phe Val
260 265 270 275

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280 285

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 85 90 95

Thr Phe Pro Val Arg Val Phe His Leu Leu Gly Val Asp Thr Leu Val
 100 105 110

Val Thr Asn Ala Ala Gly Gly Leu Asn Pro Lys Phe Glu Val Gly Asp
 115 120 125

Ile Met Leu Ile Arg Asp His Ile Asn Leu Pro Gly Phe Ser Gly Gln
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Asn Pro Leu Arg Gly Pro Asn Asp Glu Arg Phe Gly Asp Arg Phe Pro
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Thr Trp Lys Gln Met Gly Glu Gln Arg Glu Leu Gln Glu Gly Thr Tyr
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Val Met Val Ala Gly Pro Ser Phe Glu Thr Val Ala Glu Cys Arg Val
 195 200 205

Leu Gln Lys Leu Gly Ala Asp Ala Val Gly Met Ser Thr Val Pro Glu
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Val Ile Val Ala Arg His Cys Gly Leu Arg Val Phe Gly Phe Ser Leu
 225 230 235 240

Ile Thr Asn Lys Val Ile Met Asp Tyr Glu Ser Leu Glu Lys Ala Asn
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 Ile Lys Tyr Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val
 15 20 25

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 Ser His Tyr Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser
 30 35 40 45

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 Phe Ser Val Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val
 80 85 90

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 Thr Ile Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp
 95 100 105

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 110 115 120 125

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 Gly Asp Trp Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr
 130 135 140

atc ccg agc aat tat gta gcg cct gca gat tcc att cag gca gaa gaa 481
 Ile Pro Ser Asn Tyr Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu
 145 150 155

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 Trp Tyr Phe Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Leu
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caa aca gaa cta gta aca aag ggc cga gtg cca tat cca ggt atg gtg 1441
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 465 470 475

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<212> PRT

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<213> Homo sapiens

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Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ser Ala Lys
 35 40 45

Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly
 50 55 60

Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser Phe Ser Val
 65 70 75 80

Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val Thr Ile Phe
 85 90 95

Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe
 100 105 110

Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp
 115 120 125

Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr Ile Pro Ser
 130 135 140

Asn Tyr Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu Trp Tyr Phe
 145 150 155 160

Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Leu Asn Pro Gly
 165 170 175

Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly
 180 185 190

Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Glu Ile Arg Gly Asp Asn
 195 200 205

Val Lys His Tyr Lys Ile Arg Lys Leu Asp Asn Gly Gly Tyr Tyr Ile
 210 215 220

Thr Thr Arg Ala Gln Phe Asp Thr Leu Gln Lys Leu Val Lys His Tyr
 225 230 235 240

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Thr Glu His Ala Asp Gly Leu Cys His Lys Leu Thr Thr Val Cys Pro
 245 250 255

Thr Val Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp Ala Trp Glu Ile
 260 265 270

Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly Cys Phe
 275 280 285

Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys Val Ala Ile
 290 295 300

Lys Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln Glu
 305 310 315 320

Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val Pro Leu Tyr
 325 330 335

Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe Met Ser
 340 345 350

Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly Lys Tyr Leu
 355 360 365

Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met
 370 375 380

Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala
 385 390 395 400

Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala Asp Phe Gly
 405 410 415

Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala
 420 425 430

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg
 435 440 445

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Gln Thr Glu
 450 455 460

Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu
 465 470 475 480

Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly
 485 490 495

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Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp
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Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp
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Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn Leu
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 uacaguguca ccauguccgu caucuucagc aaaggaaca gcaguuaau ucagcagucu 180
 uucaugaca ccauuauggag gauccucagg gguaacgccu uuuggaggug caucuuccc 240
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cuauuaaaaa aaaaaaaaaa aaa

4343